



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lonsdale, John
Milner, Peter
Payne, David
Pearson, Stewart

(ii) TITLE OF THE INVENTION: Novel FabI

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 28-August-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/024845
(B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

00750043 01 25597

(B) TELEFAX: 610-270-5090

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn
 1 5 10 15
 Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly
 20 25 30
 Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu
 35 40 45
 Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln
 50 55 60
 Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile
 65 70 75 80
 Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe
 85 90 95
 Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu
 100 105 110
 Gly Phe Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val
 115 120 125
 Ala His Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala
 130 135 140
 Thr Thr Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met
 145 150 155 160
 Gly Val Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu
 165 170 175
 Asp Leu Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro
 180 185 190
 Ile Arg Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu
 195 200 205
 Lys Glu Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val
 210 215 220

Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
225					230					235					240
Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTAAATC	TTGAAAACAA	AACATATGTC	ATCATGGGAA	TCGCTAATAA	GCGTAGTATT	60
GCTTTTGGTG	TCGCTAAAGT	TTTAGATCAA	TTAGGTGCTA	AATTAGTATT	TACTTACCGT	120
AAAGAACGTA	GCCGTAAAGA	GCTTGAAAAA	TTATTAGAAC	AATTAAATCA	ACCAGAAGCG	180
CACTTATATC	AAATTGATGT	TCAAAGCGAT	GAAGAGGTTA	TTAATGGTTT	TGAGCAAATT	240
GGTAAAGATG	TTGGCAATAT	TGATGGTGTA	TATCATTCAA	TCGCATTTGC	TAATATGGAA	300
GACTTACGCG	GACGCTTTTC	TGAAACTTCA	CGTGAAGGCT	TCTTGTTAGC	TCAAGACATT	360
AGTTCTTACT	CATTAACAAT	TGTGGCTCAT	GAAGCTAAAA	AATTAATGCC	AGAAGGTGGT	420
AGCATTGTTG	CAACAACATA	TTTAGGTGGC	GAATTCGCAG	TTCAAAATTA	TAATGTGATG	480
GGTGTTGCTA	AAGCGAGCTT	AGAAGCAAAT	GTAAATATT	TAGCATTAGA	CTTAGGTCCT	540
GATAATATTC	GCGTTAATGC	AATTTAGCT	GGTCCAATCC	GTACATTAA	TGCAAAAGGT	600
GTGGGTGGTT	TCAATACAAT	TCTTAAAGAA	ATCGAAGAGC	GTGCACCTTT	AAAACGTAAC	660
GTTGATCAAG	TAGAAGTAGG	TAAAACAGCG	GCTTACTTTR	TAAGTGACTT	ATCAAGTGGC	720
GTTACAGGTG	AAAATATTCA	TGTAGATAGC	GGATTCCACG	CAATTAAATA	A	771